SEQUENCE LISTING

<110> Gilbertson, Debra G.

<120> METHOD OF TREATING FIBROSIS

<130> 00-53

<160> 18

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<213> Homo sapiens

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<222> (154)...(1191)

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cgccgtgagt gagctctcac cccagtcagc caa atg agc ctc ttc ggg ctt ctc      174
                                     Met Ser Leu Phe Gly Leu Leu
                                      1               5

ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa       222
Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu
        10                  15                  20

tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac       270
Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn
    25                  30                  35

gga gta caa gat cct cag cat gag aga att att act gtg tct act aat       318
Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn
 40                  45                  50                  55
gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg       366
Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr
                 60                  65                  70
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gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa 414
Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln
75 80 85

ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata 462
Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile
90 95 100

tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata 510
Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile
105 110 115

tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct 558
Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
120 125 130 135

aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct 606
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro
140 145 150

tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc 654
Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe
155 160 165

aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg 702
Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu
170 175 180

gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt 750
Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu
185 190 195

att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta 798
Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu
200 205 210 215

tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga 846
Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg
220 225 230

aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta 894
Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu
235 240 245

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tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta      942
Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu
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aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc      990
Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg
    265                 270                 275

tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa     1038
Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln
280                 285                 290                 295

tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg     1086
Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu
                300                 305                 310

aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg     1134
Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val
            315                 320                 325

gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca     1182
Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr
        330                 335                 340

gga gga tag ccgcatcacc accagcagct cttgcccaga gctgtgcagt             1231
Gly Gly  *
    345

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agaattagga gttgtgcaac agctcttttg agaggaggcc taaaggacag gagaaaaggt   1411
cttcaatcgt ggaaagaaaa ttaaatgttg tattaaatag atcaccagct agtttcagag   1471
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aactctaaag ctccatgtcc tgggcctaaa atcgtataaa atctggattt ttttttttt    1651
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<213> Homo sapiens

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Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	His	Glu	Arg
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Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	Pro	Arg	Phe	Pro
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His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	Arg	Leu	Val	Ala	Val
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Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	Asp	Glu	Arg	Phe	Gly	Leu
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Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	Tyr	Asp	Phe	Val	Glu	Val	Glu
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Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr
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Val	Pro	Gly	Lys	Gln	Ile	Ser	Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe
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Val	Ser	Asp	Glu	Tyr	Phe	Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr
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Asn	Ile	Val	Met	Pro	Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu
				165					170					175	
Pro	Pro	Ser	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala
			180					185					190		
Phe	Ser	Thr	Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp
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Gln	Leu	Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly
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Lys	Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu
225					230					235					240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	Ser
				245					250					255	
Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	Trp	Pro
			260					265					270		
Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	Cys	Cys	Leu
		275					280					285			
His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	Val	Thr	Lys	Lys
	290					295					300				
Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	Gly	Val	Arg	Gly	Leu
305					310					315					320
His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	His	His	Glu	Glu	Cys	Asp
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ctgcgccagc acctgttggc ccgccagctg gccgcccgcg ccccccgcgc cccccgcgcc    180
cgcccggccg ccagccccgc gccccgcgcg ccgcccgctg ggggaaagtg gagacgggga    240
ggggacaaga gcgatcctcc aggccagcca ggccttccct tagccgcccg tgcttagccg    300
ccacctctcc tcagccctgc gtcctgccct gccttagggc aggcatccga gcgctcgcga    360
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ctccccccag gtgggggtgg ggcgccgcct gccgccccga tcagcagctt tgtcattgat    600
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cgagtgagcc ctcgccccag tcagccaa atg ctc ctc ctc ggc ctc ctc ctg      1072
                               Met Leu Leu Leu Gly Leu Leu Leu
                                1               5

ctg aca tct gcc ctg gcc ggc caa aga acg ggg act cgg gct gag tcc     1120
Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser
    10                  15                  20

aac ctg agc agc aag ttg cag ctc tcc agc gac aag gaa cag aac gga     1168
Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly
25                  30                  35                  40

gtg caa gat ccc cgg cat gag aga gtt gtc act ata tct ggt aat ggg     1216
Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly
                45                  50                  55
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agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg     1264
Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val
            60                  65                  70

ctg gtg tgg aga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg     1312
Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu
        75                  80                  85

aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc     1360
Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys
    90                  95                  100

aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta     1408
Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu
105                 110                 115                 120

gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa     1456
Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys
                125                 130                 135

gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct     1504
Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser
            140                 145                 150

gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca     1552
Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr
        155                 160                 165

gaa acc acg agt cct tcg gtg ttg ccc cct tca tct ttg tca ttg gac     1600
Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp
    170                 175                 180

ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att     1648
Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile
185                 190                 195                 200

cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac     1696
Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr
                205                 210                 215

aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa     1744
Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys
            220                 225                 230
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agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac 1792
Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr
235 240 245

agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag 1840
Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys
250 255 260

agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt 1888
Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys
265 270 275 280

gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt 1936
Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys
285 290 295

gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga 1984
Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg
300 305 310

cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct 2032
Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala
315 320 325

ctg gaa cac cac gag gaa tgt gac tgt gtg tgt aga gga aac gca gga 2080
Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Asn Ala Gly
330 335 340

ggg taa ctgcagcctt cgtagcagca cacgtgagca ctggcattct gtgtaccccc 2136
Gly *
345

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gtatggacat atcctattta tttcaatact agggttttat tacctttaaa ctctgctcca   3336
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taatctgtgc ccaagttttg tggtgactat ttgaattaaa atgtattgaa tcatcaaata   3516
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<213> Mus musculus

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Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
        35                  40                  45
Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
    50                  55                  60
His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
65                  70                  75                  80
Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
                85                  90                  95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
            100                 105                 110
Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
        115                 120                 125
Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
    130                 135                 140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                 150                 155                 160
Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu
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Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala
            180                 185                 190
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Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
        195                 200                 205
Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
    210                 215                 220
Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu
225                 230                 235                 240
Leu Lys Glu Glu Val Lys Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
                245                 250                 255
Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
            260                 265                 270
Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
        275                 280                 285
His Asn Cys Asn Glu Cys Gln Cys Val Pro Arg Lys Val Thr Lys Lys
    290                 295                 300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu
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His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
                325                 330                 335
Cys Val Cys Arg Gly Asn Ala Gly Gly
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<212> PRT
<213> Homo sapiens

<400> 5

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            20                  25                  30
Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
        35                  40                  45
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
    50                  55                  60
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65                  70                  75                  80
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
                85                  90                  95
Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
            100                 105                 110
Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
        115                 120                 125
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Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145 150 155 160

Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
165 170 175

Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
180 185 190

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
195 200 205

Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
210 215 220

Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
225 230 235 240

Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
245 250 255

Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
260 265 270

Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
275 280 285

Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
290 295 300

Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
305 310 315 320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
325 330 335

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Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
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Pro Arg
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